

Ultrasound image segmentation using a point distribution model in a Bayesian framework

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Abstract

An empirical Bayes framework is used to incorporate point distribution models (PDMs) within Bayesian image analysis, thus synthesising two approaches to the fitting of stochastic templates. Manually-segmented images are used to identify both a PDM and a likelihood function, leading to a posterior distribution from which inferences can be drawn. The methodology is explored and illustrated using 144 ultrasound images of sheep. Estimates of sheep fat and muscle depths are shown to be comparable in accuracy with manual interpretation of images.

1 Introduction

Templates are examples of objects to be located in images. The use of rigid templates is well established, but is usually inadequate in biological applications where natural variability ensures that shapes are not identical. Stochastic, or deformable, templates generalise rigid templates by allowing variation within prescribed probability distributions. Two methodologies have recently emerged in the machine vision and statistical literature, each with distinct strengths and weaknesses.

- The machine vision approach is based on point distribution models (PDMs), which are extracted from manually-interpreted training images, and used to specify active shape models (ASMs) which are fitted to new images to match edges [1, and references therein].
- The statistical approach is a type of Bayesian image analysis, where a prior model specifies what is expected in an image. This is combined with the likelihood of an observed image conditional on the model, resulting in a posterior distribution from which inferences can be drawn [2, 3].

The strength of the machine vision approach is the ease of template formation, whereas the statistical approach provides a powerful set of tools for fitting a template to data.

This paper reports an experiment in applying Empirical Bayes Methods [4] to gain the benefits of both approaches. (See [5] for an alternative approach.)

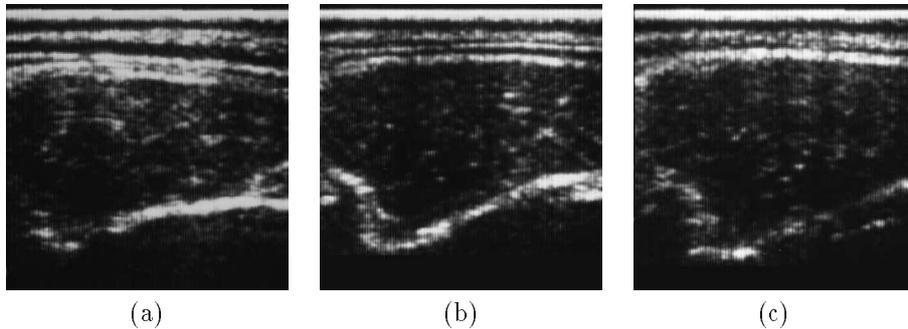


Figure 1: *Ultrasound images of the backs of three sheep.*

In §2, ultrasound images of sheep are introduced (see Figure 1), which present a challenging problem for automatic segmentation. In §3, training data, in the form of manually-specified templates, are used to identify a PDM for use as a prior distribution. Bayes' theorem is used to combine the PDM with a likelihood function of simple form, but the resulting posterior distribution has a mode which does not consistently coincide with the parameter values in the original template. Therefore, in §4, a new method is proposed in which the training data are further used to modify the likelihood function. Results, given in §5 for the training data and a validation data set, show that sheep fat and muscle depths are estimated as accurately as for manual interpretation. Finally, in §6, generalisations of the method are discussed.

2 Ultrasound images

Non-invasive imaging techniques such as ultrasound, X-ray computed tomography (CT) and magnetic resonance imaging (MRI) are ubiquitous in hospitals. They are also used increasingly in animal science and production to predict body composition [6]. In particular, ultrasound has become widely used in animal breeding to assist in selection for leaner carcasses, because it uses cheaper and more-mobile imaging equipment than either X-ray CT or MRI. Unfortunately, ultrasound images are far more susceptible to noise and are therefore far harder to interpret, as can be seen in Figure 1. This is particularly true in this application, because we are using an old instrument which lacks a video output. The instrument operates by sending a pulse of sound waves of very high frequency into a subject (a 'squeak', about 250 times the highest frequency audible to the human ear). When the sound wave meets a boundary between two tissues, partial reflection occurs. The greater the difference in acoustic impedance between the two tissues, the greater the reflection. For example, more energy is reflected from a muscle-bone interface than from a muscle-fat one. This faint echo is received by the instrument and converted into electrical signals which are displayed on a video monitor, with time delay interpreted as depth.

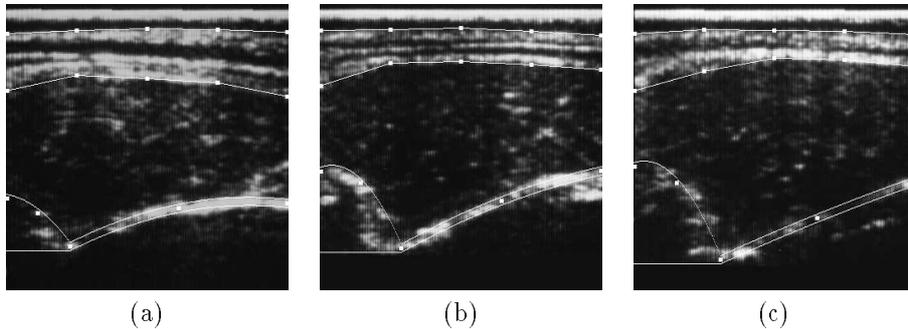


Figure 2: *Ultrasound images from Figure 1 with manually-identified boundaries superimposed.*

A Vetscan ultrasonic instrument was used to scan the backs (at the 13th thoracic vertebra) of each of 72 Suffolk ewe lambs on two consecutive weeks [7]. A subset of the images, the pairs from 24 sheep, were interpreted manually, by using a mouse to control a screen cursor and identify 4 tissue boundaries. For example, Figure 2 shows manually-identified boundaries for the images in Figure 1. The topmost piecewise-linear line locates the boundary between the skin (above) and the fat (below). The piecewise-linear line below this identifies the fat-muscle boundary. Finally, the two lowest lines, which are piecewise-quadratic, show the top and bottom of a rib and, on the left of each image, part of the backbone.

The aim of the image interpretation is to estimate the average fat depth and maximum muscle depth for each sheep, from which whole body composition can be estimated. Obtaining these measurements manually is a slow and tedious task, and the results will vary between scientists. It is desirable to fully automate the analysis. Some success has been achieved with low-level image processing algorithms [7], but these are unlikely to generalise easily to other scanners, sheep breeds or scanning positions. Trainable models have been applied in the interpretation of human echocardiograms [8]. Therefore, the segmentation problem looks well suited for stochastic templates, whereby high-level knowledge on anatomical structure can be incorporated into a segmentation algorithm.

3 Empirical Bayes approach

The templates can be summarised by 15 landmark points, which are also shown in Figure 2. The top 10 points specify the top and bottom of the fat boundary, while the bottom 5 points specify the rib and backbone. In the latter case, quadratic interpolation has been used and the rib is constrained to a fixed width. 16 parameters are required to specify the 15 landmarks, namely 15 row locations, together with the column location where the rib joins the backbone. The remaining 14 column locations are fixed, or defined relative to this single column location.

We assessed the 16 parameters for multivariate normality. Figure 3 shows

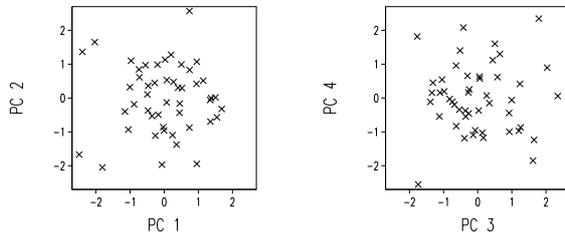


Figure 3: Scatter plot of principal component scores for 48 training images: (a) first v. second, (b) third v. fourth.

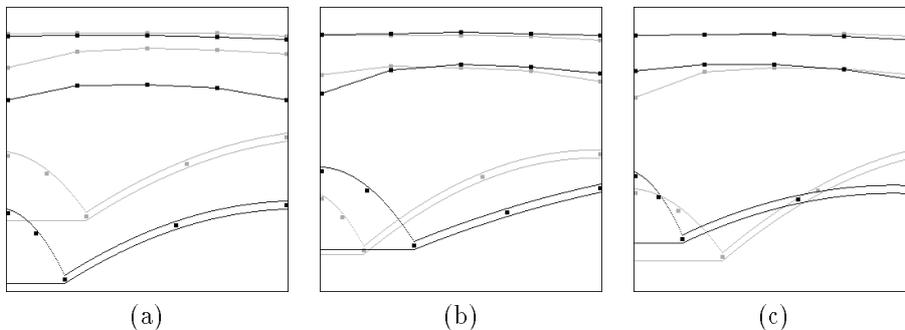


Figure 4: Average template +2 standard deviations (solid line) and average template -2 standard deviations (dotted line) for: (a) first, (b) second and (c) third principal component.

scatter plots for the first 4 principal components, which account for 91% of the variability. The plots support the normality hypothesis, as do normal probability plots (not shown). Therefore, we assume that the prior probability can be specified by

$$P(\beta) \propto \exp \left[-\frac{1}{2} \beta^T \beta \right],$$

where β denotes the vector of (however many) principal components we choose to use. Figure 4 shows the effects of the first 3 principal components on the template. As can be seen, the first principal component mainly affects fat depth, the second one specifies the position of the scan relative to the backbone and the third one changes rib angle.

If the top-most black and light-grey bands in the images (the first 18 rows of each image, which show the transducer-skin boundary) are ignored, the templates in Figure 2 partition the images into 5 segments, corresponding to: (1) skin, (2) fat, (3) muscle, (4) bone and (5) internal organs. For simplicity, pixels in segment k

	μ_1	μ_2	μ_3	μ_4	μ_5	σ_1	σ_2	σ_3	σ_4	σ_5
estimates	77	120	31	65	20	57	64	26	63	16
modified values	-68	2	-20	84	19	49	67	45	99	27

Table 1: Values of parameters in likelihood.

are assumed to be independently, identically, normally distributed with mean μ_k , standard deviation σ_k . Therefore, the likelihood of the image, conditional on a template specified by β , is given by

$$P(y|\beta) \propto \prod_i \prod_j \frac{1}{\sigma_{f_{i,j}}} \exp \left[-\frac{1}{2\sigma_{f_{i,j}}^2} (y_{i,j} - \mu_{f_{i,j}})^2 \right],$$

where $y_{i,j}$ is the pixel value in row i column j of the image and $f_{i,j}$ denotes its segment label (between 1 and 5). The independence assumption is clearly inappropriate, because correlations between adjacent pixels are evident in Figure 1, but has been used by others [3], so we will start by using it here. Alternatively, we could have tried using the ASM methodology [1] to align edges, but the presence of multiple and very noisy edges in the images made us favour a statistical approach.

For computational efficiency, $\log [P(y|\beta)]$ can be re-expressed as

$$-\sum_{k=1}^5 \log(\sigma_k) \sum_j (g_{j,k} - g_{j,k-1}) - \sum_{k=1}^5 \frac{1}{2\sigma_k^2} \sum_j \left((A_{g_{j,k},j} - A_{g_{j,k-1},j}) - 2(B_{g_{j,k},j} - B_{g_{j,k-1},j})\mu_k + (g_{j,k} - g_{j,k-1})\mu_k^2 \right),$$

where $g_{j,k}$ denotes the last row of segment k in column j , $g_{j,0}$ is set to 18,

$$A_{g,j} = \sum_{i=0}^g y_{i,j}^2 \quad \text{and} \quad B_{g,j} = \sum_{i=0}^g y_{i,j},$$

which can be computed recursively down each column, by

$$A_{g,j} = A_{g-1,j} + y_{g,j}^2 \quad \text{and} \quad B_{g,j} = B_{g-1,j} + y_{g,j}.$$

Both f and g are functions of β , but, to prevent the notation from becoming too complicated, this dependence has not been indicated.

Parameters μ_k and σ_k can be estimated from the 48 training images, as the sample means and standard deviations of pixel values $y_{i,j}^{(u)}$ for which $f_{i,j}^{(u)} = k$, where $u = 1 \dots 48$ indexes the 48 images. This is equivalent to maximising $\prod_u P(y^{(u)}|\beta)$. These estimates are given in the first row of Table 1. All images were standardised to have the same mean intensity, and pixel values range from 0 to 255, with 0 corresponding to black and 255 to white. As we would expect from inspection

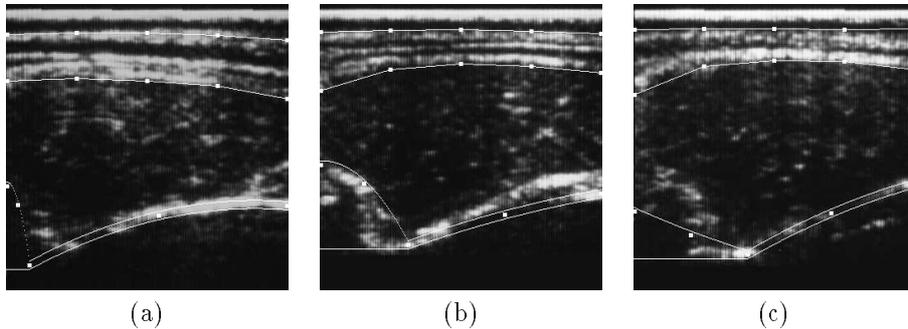


Figure 5: *Ultrasound images from Figure 1, together with poorly located boundaries based on simplistic likelihood function.*

of the images, segment 2 (the fat layer) has the highest mean pixel value, and segments 2 and 4 (fat and bone) have the largest standard deviations.

Bayes' theorem gives a posterior probability for the template, conditional on an image, proportional to the product of the prior probability and the likelihood, that is,

$$P(\beta|y) \propto P(\beta)P(y|\beta),$$

where ‘|’ denotes ‘conditional on’. It would have been possible to place prior distributions on μ and σ , but we found it to be simpler and as effective to keep them fixed. The Bayesian framework also gives us the option to explore the full posterior distribution to assess the range of templates compatible with an image, but at present we have concentrated solely on the distribution mode.

We maximised $P(\beta|y^{(u)})$ for each of the 48 images in the training set, using the Nelder-Mead optimisation algorithm from 20 starting positions, each being the best of 100 randomly chosen values from the prior distribution for β . We also experimented with alternative optimisation methods, in particular the use of Markov Chain Monte Carlo [3], but found this to be more effective for studying the posterior distribution than for simply finding the mode. The results we present are based on using 4 principal components only. Very similar results were obtained using more components, but would not extend so readily to the approach taken in §4 and so are not given here. Although the manual template was approximately recovered in most cases, this was not consistently the case. Figure 5 shows results for 3 images. In particular, it can be seen in Figure 5(b) that the rib has been misplaced. The algorithm also had trouble locating the backbone, but we are less surprised by this because information on the backbone is very sparse in the ultrasound images. Overall, average fat depths obtained from the algorithm agreed well with those from the manual template, with a sample correlation coefficient of 93%, but maximum muscle depths agree less well, with a correlation of 24%.

4 Modified likelihood

The problem arises from the likelihood we have assumed, which dominates $P(\beta)$ in the expression for $P(\beta|y)$ but provides only a rough approximation to the distribution of y . We found that the templates were recovered more consistently if the likelihood was modified in an *ad hoc* way by increasing σ_5 so that bright features below the rib were less influential, and downweighting the likelihood by

$$P(\beta|y) \propto P(\beta)P(y|\beta)^\gamma.$$

We then made this approach more systematic, by searching for values of μ_k , σ_k and γ to optimise the recovery of the templates, by maximising the criterion

$$\frac{\bar{X}}{\sqrt{\frac{1}{47} \sum_u (X^{(u)} - \bar{X})^2}},$$

where u indexes the 48 training images,

$$X^{(u)} = \log P(\beta^{(u)}|y^{(u)}) - \max_{\beta' \in S^{(u)}} [P(\beta'|y^{(u)})], \quad \bar{X} = \frac{1}{48} \sum_u X^{(u)},$$

and $S^{(u)}$ is the set of integer values of β' within 3 standard deviations of the mean template, but excluding those values near $\beta^{(u)}$, i.e.

$$\{\beta' \text{ such that } \beta'_i = \pm 3, \pm 2, \pm 1, 0 \text{ for } i = 1 \dots 4; \text{ and } \max_i |\beta'_i - \beta_i^{(u)}| \geq 1\},$$

which has $7^4 - 2^4 = 2385$ elements. Alternatively, randomly-selected values of β' could have been used. Ideally, we would like all the $X^{(u)}$ to be positive, because then $P(\beta^{(u)}|y^{(u)})$ would be larger than $P(\beta'|y^{(u)})$ for any other value of β' . The criterion we used is a differentiable measure of positivity of the X 's which is invariant to multiplying factors in the probabilities.

The Nelder-Mead optimisation algorithm was used from multiple starting points. The maximum value found for the criterion was 1.01, which, if the X 's are approximately normally distributed, implies that in 16% of cases X will be negative. For comparison, the criterion was only -0.26 for the original set of parameters. The new values are given in the second row of Table 1, and $\gamma = 0.0058$. These values can be seen to be quite different from the first set, and to make no physical sense because pixels do not take negative values. Therefore, the likelihood should be regarded as an empirically-derived cost function. We also experimented with other functional forms for the likelihood, but found none better, and so retained the original form because of its computational convenience.

5 Results

The posterior probability based on the modified likelihood was again maximised for each of the 48 images in the training set, using the Nelder-Mead optimisation algorithm. The results are much improved, as can be seen in Figure 6,

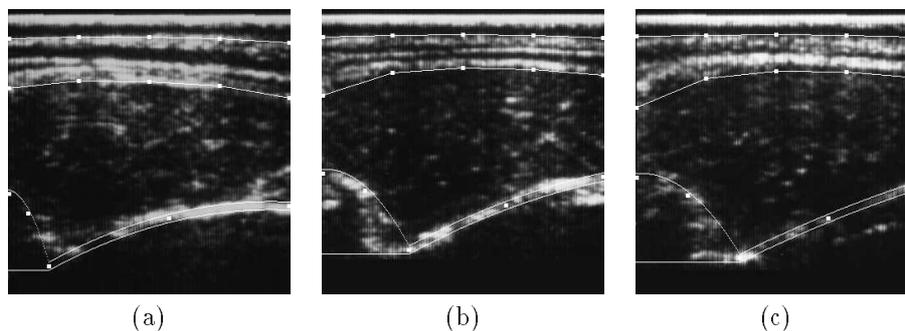


Figure 6: *Ultrasound images from Figure 1, together with boundaries based on modified likelihood function.*

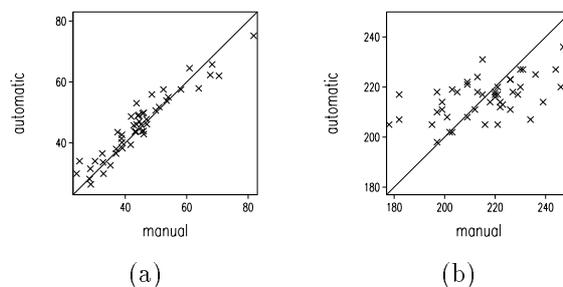


Figure 7: *Depths identified by algorithm plotted against those in manual template, for the training data: (a) average fat depth, (b) maximum muscle depth.*

although they are less than perfect: the maximum muscle depth is overestimated in Figure 6(a), as is the fat depth in Figure 6(c). Agreement between manual and automatic results is better than before: the correlation is 95% for average fat depths (Figure 7(a)), and 52% for maximum muscle depths (Figure 7(b)). Note that, correlations were not calculated on a leave-one-out basis, which would have involved recomputing the modified likelihood parameters 48 times.

For these data we do not know the true depths. However, we get some indication of the accuracy of the methods by comparing results for weeks 1 and 2 for the same sheep. Figures 8(a) and (b) show average fat depth for the manual and automatic methods. It can be seen that the manual results are more consistent, with a correlation between weeks of 97%, while the automatic method has a correlation of 91%. The situation is reversed for muscle depth, shown in Figures 9(a) and (b). Here the automatic method, with a correlation between weeks of 72%, is far superior to the 24% for the manual method. (Note that there is growth between weeks in both fat and muscle depths.)

The algorithm was applied to a validation data set consisting of pairs of images

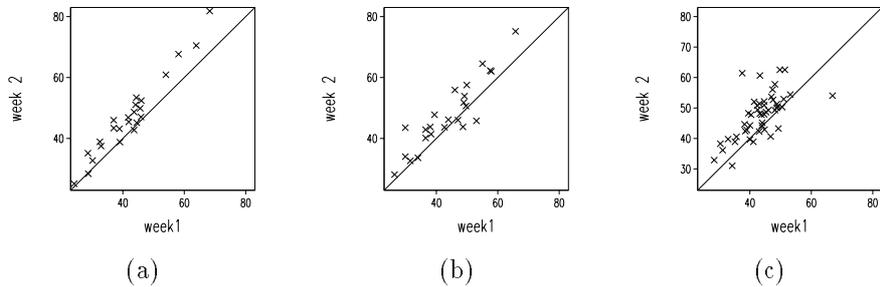


Figure 8: *Average fat depth for week 1 plotted against that for week 2, obtained using: (a) manual template applied to training data, (b) algorithm applied to training data (c) algorithm applied to validation data.*

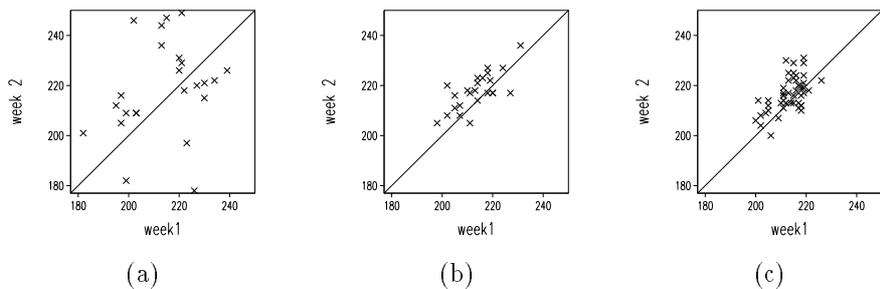


Figure 9: *Maximum muscle depth for week 1 plotted against that for week 2, obtained using: (a) manual template applied to training data, (b) algorithm applied to training data (c) algorithm applied to validation data.*

of a further 48 sheep. As is to be expected, the fit is not quite so good as for the training data. Figure 8(c) shows average fat depth for weeks 1 v 2, for which the correlation is 65%. Figure 9(c) shows muscle depth, with a correlation of 58% which is still larger than the 24% produced by the manual method on the training data. These results are good, when the poor quality of the original images are borne in mind, and estimates of sheep fat and muscle depths are comparable in accuracy with manual interpretation of images.

6 Discussion

We have demonstrated how training data can be used in an Empirical Bayes approach to identify, not only the prior distribution, but also the likelihood function such that the mode of the posterior density coincides with the template. Thus, we have maximised the amount of information obtained from the training data.

Alternative approaches would be to attempt to model the image more systematically, for example, by taking into account correlations between pixels in the same segment, or to repeatedly return to each training image and modify the fitting strategy until all images are correctly segmented.

Further work is needed to explore alternative fitting strategies using Markov Chain Monte Carlo methods to estimate the posterior distribution. Experience is needed in applying the method to sheep of other breeds and to scans obtained at other anatomical locations, such as the lumbar region where the fat boundary has a different shape and ribs are absent. We will develop the methodology, and extend it to handle hierarchical structures[3], to segment X-ray CT images of sheep. We also intend to place this work in the wider context of *semi-automatic image analysis*, an area much neglected from a methodological perspective.

Acknowledgements

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